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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.45349 Seconds
(Without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613b-13

Perfect score: 582

Sequence: 1 MSMDLTFQKKHLTNRDVC.....TFCVTCENQAPVHFVGWGHG 105

Scoring table: BLCSUM62

Searched: Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	94.7	104	1	RR30_RANPI
2	287	49.3	111	1	RNPQ_RANCA
3	280.5	48.2	111	1	LECS_RANCA
4	264.5	45.4	111	1	RNPQ_RANCA
5	144	24.7	119	1	RNP_IGUG
6	132	23.7	124	1	RNP_GALMU
7	130.5	22.4	145	1	ANGR_MOUSE
8	130.5	22.4	146	1	ANGI_CERAE
9	128	23.0	148	1	ANGI_BOVIN
10	126	21.6	128	1	RNP_MYOCO
11	125	21.5	124	1	RNP_BALAC
12	121.5	20.9	146	1	ANGI_MACMU
13	120	20.6	128	1	RNP_CAVPO
14	120	20.6	128	1	RNP_PROGU
15	119.5	20.5	145	1	ANGI_MOUSE
16	118.5	20.4	146	1	ANGI_PAPHA
17	118	20.3	124	1	RNP_CHIR
18	117	20.1	128	1	RNP_HYDHY
19	116	19.9	125	1	ANGI_RABIT
20	115	19.8	146	1	ANGI_MIOTA
21	114	19.6	124	1	RNP_HIPAM
22	113	19.4	147	1	ANGI_HUMAN
23	113	19.4	147	1	ANGI_PANTR
24	113	19.4	156	1	ECPP_MOUSE
25	112	19.2	124	1	RNP_PIG
26	112	19.2	128	1	RNP_HYSCR
27	112	19.2	156	1	RNP_BOVIN
28	112	19.2	156	1	RNP_MYOGI
29	111.5	19.2	147	1	RNL4_HUMAN
30	111	19.1	128	1	RNP_HORSE
31	111	19.1	146	1	ANGI_SAISC
32	111	19.1	167	1	RNBR_BOVIN
33	110.5	19.0	123	1	ANGI_PIG

ALIGNMENTS

RESULT 1	ID	RN30_RANPI	STANDARD	PRT	104 AA.
AC	P22069				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-FEB-1995 (Rel. 31, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OS	Rana pipiens (Northern leopard frog).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCHL_TaxID=8404;				
RN	[1]				
RP	3D-STRUCTURE MODELING.				
RC	TISSUE=Embryo;				
RX	MEDLINE=91093131; PubMed=1985896;				
RA	Artelt W., Mikulski S.M., Shogen K.;				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251(1991).				
RN	[2]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=9306156; PubMed=1438177;				
RA	Mosimann S.C., Johns K.L., Artelt W., Mikulski S.M., Shogen K., James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";				
RL	Proteins 14:392-400(1992).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RX	MEDLINE=94166079; PubMed=8120892;				
RA	Mosimann S.C., Artelt W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PDB: 1ONC; 31-JAN-94.				
DR	InterPro: IPR001427; Rnasea.				
DR	Pfam: PF00074; rnaasea. 1.				
DR	Prodom: PD000535; Rnasea. 1.				
DR	SMART: SM00092; Rnase-Pc; 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.				
FT	MOD_RES	1			
FT	ACT_SITE	10	1		
FT	ACT_SITE	31	31		
FT	ACT_SITE	97	97		
FT	DISULFID	19	68		
FT	DISULFID	30	75		
FT	DISULFID	48	90		

34	110.5	19.0	155	1	ECPI_MOUSE	P97426	mus musculus
35	110	18.9	124	1	RNPA_CAVPO	P00678	cavia porcea
36	110	18.9	141	1	RNBR_GIRCA	O29542	giraffa cam
37	110	18.9	146	1	ANGI_SAOE	O8N62	seguinus oe
38	110	18.9	151	1	RNBR_AXIPR	P87350	axis porcin
39	110	18.9	156	1	ECPP2_MOUSE	P97425	mus musculus
40	109	18.7	123	1	ANGI_BOVIN	P80929	bos taurus
41	109	18.7	124	1	RNP_AEPME	P07847	aepyceros m
42	109	18.7	124	1	RNP_ANTAM	P00668	antilocapra
43	109	18.7	124	1	RNP_SHEEP	P00661	ovis aries
44	108.5	18.6	150	1	RNKG_SAISC	O46529	saimiri sci
45	108.5	18.6	155	1	ECPP_RAT	P70709	ratius norv

FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 48
 FT TURN 49 50
 FT STRAND 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SO SEQUENCE 104 AA; 11845 MM; 22A753C29E56B64 CRC64;

Query Match Best Local Similarity 94.7%; Score 551; DB 1; Length 104;
 Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 DWLTFQKHHTNTRDVCNNIMSTNLFPHCKDKNFTYSRPEPVKAICGIIASKNVLTTS 62
 DB 2 DWLTFQKHHTNTRDVCNNIMSTNLFPHCKDKNFTYSRPEPVKAICGIIASKNVLTTS 61
 OY 63 EFTLSDCNVTSRPPCKYKLRKSTNFCVTCENQAPVHFVGVGHC 105
 DB 62 EFTLSDCNVTSRPPCKYKLRKSTNFCVTCENQAPVHFVGVGHC 104

RESULT 2

RNPO_RANCA
 ID RNPO_RANCA STANDARD; PRT; 111 AA.

AC P11916;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding lectin) (SBL-C).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Egg;
 RX MEDLINE=87299649; PubMed=3304421;
 RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H.,
 RA Takayanagi G., Hakomori S.;
 RT "Amino acid sequence of stallic acid binding lectin from frog (Rana catesbeiana) eggs.";
 RL Biochemistry 26:2189-2194(1987).
 RN [2]
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.

RX MEDLINE=92220613; PubMed=1373237;
 RA Liao Y.-D.;
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
 RL Nucleic Acids Res. 20:1371-1377(1992).
 RN [3]
 RP CHARACTERIZATION.

RC TISSUE=Egg;
 RX MEDLINE=93192604; PubMed=8448385;
 RA Nitta K., Oyama F., Oyama R., Sekiuchi K., Kawachi H.,
 RA Takayanagi Y., Hakomori S., Titani K.;
 RT "Ribonuclease activity of stallic acid-binding lectin from Rana catesbeiana eggs.";
 RL Glycobiology 3:37-45(1993).
 RN [4]
 RP STRUCTURE BY NMR.

RX MEDLINE=98437383; PubMed=9761686;
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T. H.;

RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog)."
 RL J. Mol. Biol. 283:231-244(1998).
 CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C) AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN AGGLOutinATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PDB: 1BC4; 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolase; Nuclease; Endonuclease; Stallic acid; Lectin; 3D-structure.
 FT MOD_RES 1 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SO SEQUENCE 111 AA; 12464 MM; 0BC9E5F5729ECF4 CRC64;

Query Match Best Local Similarity 49.3%; Score 287; DB 1; Length 111;
 Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

OY 3 DWLTFQKHHTNTRDVCNNIMSTNLF---HCKDKNFTYSRPEPVKAICGIIASKNV 58
 DB 2 DWLTFQKHHTNTRDVCNNIMSTNLF---HCKDKNFTYSRPEPVKAICGIIASKNV 58
 OY 59 LTTSEFTSDC---NVTSPCKYKLRKSTNFCVTCENQAPVHFVGVGHC 105
 DB 61 LTTSEFTSDC---NVTSPCKYKLRKSTNFCVTCENQAPVHFVGVGHC 105

RESULT 3

LECS_RANCA
 ID LECS_RANCA STANDARD; PRT; 111 AA.

AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stallic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese redbellied frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.

RC TISSUE=Egg;
 RX MEDLINE=91035319; PubMed=2229005;
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,
 RA Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.";
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN PREFERENTIALLY AGGLOutinATES A LARGE VARIETY OF TUMOR CELLS, BUT IT DOES NOT AGGLOutinATES NON-TRANSFORMED CELLS AND ERYTHROCYTES.

CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0120; JX0120.

RESULT 4				
NRPL_RANCA	STANDARD;	PRT;	111 AA.	
ID	NRPL_RANCA			
AC	P14626			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ribonuclease, liver (EC 3.1.27.5).			
OS	Rana catesbeiana (Bull frog).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1].			
RP	SEQUENCE.			
RC	TISSUE=Liver:			
RX	MEDLINE=90130374; PubMed=26135682;			
RA	Nitta R., Katsuyama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,			
RA	Okazaki T., Ohgi K., Irie M.;			
RT	"Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)			
RT	liver.";			
RL	J. Biochem. 106:729-735(1989).			
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-			
CC	phosphates and 3'-phosphonucleotides ending in C-P or U-P			
CC	with 2',3'-cyclic phosphate intermediates.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
CC	PIR: JX0085; JX0085.			
DR	HSSP: P11916; IBC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA; 1			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_PC; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease.			
FT	MOD_RES: 1			
FT	ACT_SITE: 10			
FT	ACT_SITE: 35			
FT	ACT_SITE: 104			
FT	DISULFID: 19			
FT	DISULFID: 34			
FT	DISULFID: 52			
FT	DISULFID: 94			
FT	SEQUENCE: 111 AA; 12461 MW; D64BA72456C10768 CRC64;			

RT		"The amino acid sequence of iguana (iguana iguana) pancreatic ribonuclease";
RL	Eur. J. Biochem.	219:641-646(1994).
CC	-I-	CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
CC	-I-	SUBCELLULAR LOCATION: Secreted.
CC	-I-	TISSUE SPECIFICITY: PANCREAS.
CC	-I-	SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR	HSPB:	P00656; 1L80.
DR	InterPro:	IPIR001427; RNaseA.
DR	pfam:	PF00074; rnaSeA_1.
DR	PRINTS:	PR00794; RIBONUCLEASE.
DR	ProDom:	PD000535; RNaseA_1.
DR	SMART:	SM00092; RNase_Pc_1.
DR	PROSITE:	PS00127; RNASE_PANCREATIC_1.
KM	Hydrolase;	Nuclease; Endonuclease.
FT	MOD_RES	1
FT	DISULFID	25
FT	DISULFID	39
FT	DISULFID	57
FT	ACT_SITE	10
FT	ACT_SITE	40
FT	ACT_SITE	113
SQ	SEQUENCE	119 AA; 13324 MW; 6072FB5B7A15BD5A CRC64;
Query Match		24.7%; Score 144; DB 1; Length 119;
Best Local Similarity		30.1%; Pred. No. 1,2e-08;
Matches	34;	Conservative 19; Mismatches 44; Indels 16; Gaps 5
OY	3 DWLTFOKRLH-----TNRDVCNNIM--STNLFHCXDKMTFIYSREPKALC--KG 51	: : : : : : : : : : :
DB	2 DMSSTQNKKIIDPEPISASNPAYCDLMOMGRNLINPTKCKTRITVFVNASSELDIQVCGSSG 61	: : : : : : : : : : :
OY	52 IIAKNVLTTSE-FYLSDC---NWTSPCKTKLKKSNTFFCVTCENQAPVHF 99	: : : : :
DB	62 TFEYEDNLXDNSNESFDLTDCKNVGGTAGPASCCKYNGTPGTKRIRIACENNQPVHF 114	:
RESULT 6		
RNP_GALMU		
ID	RNP_GALMU	STANDARD; PRT: 124 AA.

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AC P00680:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Galesa musteloides (Cuis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Galea.
OX NCBI_Taxid=10146;
RN [1]
RP SEQUENCE.
RX MEDLINE=87036770; PubMed=6571219;
RA Beintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and cuis ribonuclease."
RL J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSP: P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
DR KIM Hydrolyase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES);
SQ SEQUENCE 124 AA; 13870 MW; 609C7E51A7BBA25 CRC64;

Query Match 22.7%; Score 132; DB 1; Length 124;
Best Local Similarity 30.6%; Pred. No. 2.4e-07;
Matches 38; Conservative 18; Mismatches 36; Indels 32; Gaps 7;

QY 2 SDMLTFKKHL-----TNRDVCNNIM--STNLFCKKNTFTYSRPEPKAICKG 51
DB 3 SSAMKFOQHMDSDGHPDTNIN--YCNEMVRSMTOGRCKRPVTFVHEPLEAVAVVC-- 58
QY 52 IIAASKNV-----LTTSEFYLDSCNVTSRP---CKYKLKSTNTPCVTCEN--QA 95
DB 59 --SQKNVPCKNGQNTCYQSHSSMRITDCRVTSSSKYPNCSTYMTQAQSIIVACGTPSV 116
QY 96 PVHF 99
DB 117 PVHF 120

RESULT 7
ANGR_MOUSE STANDARD; PRT; 145 AA.
AC Q64438.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes."
RL Genomics 29:200-206(1995).
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U22519; MAA91367.1; -.
DR HSP: P03950; 1A4Y.
DR MGD: MGI:104984; Angrp.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolyase; Nuclease; Endonuclease.
FT CHAIN 1 24
FT MOD_RES 25 145
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;

Query Match 22.4%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 4.2e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

QY 31 CDKNTFTYSRPEPKAIC--KGIASKNV--LTTSEFYLDSCNVTSRP---PCKYKLKS 83
DB 63 CKDVAFTFHDFTKNNIKAIGCKKSPYGRNLRISKSRFVYTTCTHGRSPRPCKRYRASKG 122
QY 84 TMTFCVTCENQAPVHF 99
DB 123 FRYITIGCNGMPVHF 138

RESULT 8
ANGI_CERAE STANDARD; PRT; 146 AA.
AC Q8WN66.
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG OR RNASE5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Cercopithecus.
OX NCBI_Taxid=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=11919285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RT primate evolution."

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RL	FEB8 Lett.	241:41-45(1988).
RN	[1]	
RP	SEQUENCE OF 24-148.	
RC	TISSUE-plasma;	
RX	MEDLINE=89375344; Pubmed=2775757;	
RA	Bond M.D., Strydum D.J.;	
RT	"Amino acid sequence of bovine angiogenin.";	
RL	Biochemistry 28:6110-6113(1989).	
RN	[4]	
RP	CHARACTERIZATION, AND SEQUENCE OF 25-55.	
RC	TISSUE-plasma;	
RX	MEDLINE=89118214; Pubmed=3064806;	
RA	Bond M.D., Vallée B.L.;	
RT	"Isolation of bovine angiogenin using a placental ribonuclease inhibitor binding assay.";	
RL	Biochemistry 27:6282-6287(1988).	
RN	[5]	
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).	
RX	MEDLINE=95224057; Pubmed=7708754;	
RA	Acharya K.R., Shapiro R., Riordan J.F., Vallée B.L.;	
RT	"Crystal structure of bovine angiogenin at 1.5-A resolution.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).	
RN	[6]	
RP	STRUCTURE BY NMR.	
RX	MEDLINE=96280645; Pubmed=8688423;	
RA	Léquin O., Albaret C., Bonlems G., Spik G., Lallemand J.-Y.;	
RT	"Solution structure of bovine angiogenin by IH nuclear magnetic resonance spectroscopy.";	
RL	Biochemistry 35:8870-8880(1996).	
CC	-I- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS: ONCE BOUND, ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOENIN INDICES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS. BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.	
CC	-I- SUBCELLULAR LOCATION: Secreted.	
CC	-I- TISSUE SPECIFICITY: SERUM, AND MILK.	
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.	
CC	-I- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL collabration - the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announcement or send an email to license@isb-sib.ch).	
CC	EMBL: AF135124; MAG47631.1; .	
DR	PIR: A32474; A32474.	
DR	PDB: IAG1; 03-APR-96.	
DR	PDB: IGI0; 07-DEC-96.	
DNR	InterPro: IPRO01427; RNaseA.	
DNR	pfam: PF00074; rnasea; 1-	
DR	PRINTS: PR00794; RIBONUCLEASE.	
DR	Prodom: PD000535; RNaseA; 1.	
DR	SMART: SMO0092; RNase_Pc; 1.	
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.	
KW	Hydrolase; Nuclease; Endonuclease; Angiogenesis; Protein synthesis inhibitor; Signal; 3D-structure.	
FT	SIGNAL	1 23
FT	CHAIN	24 148
FT	ACT_SITE	37 37
FT	ACT_SITE	64 64
FT	ACT_SITE	138 138
FT	DISULFID	50 105
FT	DISULFID	63 116
FT	DISULFID	81 131
SQ	SEQUENCE	148 AA; 16969 MW; B7999124CBB523DD CRC64;
Query Match	22.0%; Score 128; DB 1; Length 148;	
Best Local Similarity	34.0%; Pred No. 7; 9e-07;	

RESULT 11
RNP_BALAC

NCBI TaxID=9544;
[1]

RP SEQUENCE FROM N.A. PubMed=11919285;
 RA MEDLINE=21918422;
 RA Zhang J., Rosenberg H.F.;
 RT "diversifying selection of the tumor-growth promoter angiogenin in
 RT primate evolution";
 RL Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A "RNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOENIN INDICES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AF41667; AAL61649.1;
 KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal.
 FT SIGNAL 1 24 BY SIMILARITY.
 FT CHAIN 25 146 ANGIOENIN.
 FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT ACT_SITE 37 37 BY SIMILARITY.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DISULFID 50 105 BY SIMILARITY.
 FT DISULFID 63 116 BY SIMILARITY.
 FT DISULFID 81 131 BY SIMILARITY.
 SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;
 Query Match 20.9%; Score 121.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred No. 3.8e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;
 QY 6 TFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSPPEVKAIC---KGIIASKNV-LTT 61
 DB 53 TMRERHLTSP-----CKDINTEFHCHNRHHTFALCGDEMGSPYGNLRIST 97
 QY 62 SEFTLSDCQNTS---RCKYKYLKSTNTFCVTCENQAPVH 98
 DB 98 SPFWTCKLRGSPRPPCOYRATGSRNIVVCGENGLPWH 138
 RESULT 13
 RNPB_CAVPO STANDARD; PRT; 128 AA;
 ID RNPB_CAVPO
 AC P00679;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic B (EC 3.1.27.5) (Rnase IB).
 OS Cavia porcellus (Guinea pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 CC NCBI_TaxId=10141;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=77185023; PubMed=862624;
 RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastria W.,
 RA Beutema J.J.;
 RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
 RT structure and glycosylation";
 RL Eur. J. Biochem. 75:91-100(1977).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00826; NRGPB.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaaseA. 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA. 1.
 DR SMART: SM00092; RNase_Pc. 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC. 1.
 KM Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 72 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT CARBOHD 21 21 N-LINKED (GLCNAC. . .).
 FT CAROHD 34 34 L->P.
 FT VARIANT 64 64
 SQ SEQUENCE 128 AA; 14406 MW; A2E4101A1A33E93B CRC64;
 Query Match 20.6%; Score 120; DB 1; Length 128;
 Best Local Similarity 28.5%; Pred No. 4.8e-06;
 Matches 35; Conservative 21; Mismatches 37; Indels 30; Gaps 7;
 QY 2 SDMLTFQKKHL-----TNTRDVCNNIM---STNLFHCKDKNTFYSPPEVKAICGKI 52
 DB 3 SSAMKFRQHMDEPSNSSNY-CNVMMIRRMNMGRCCKPVNTFVHESLAVQAVC--- 58
 QY 53 TSKNVL-----TTSEYFLSDCQNTSP---CKYKAKKSTNTFCVTCENQ--AP 96
 DB 59 -FQKNVLCKNGQTCNGYSRMRITDCRVTSKSSKFPNCGRYSNOAKSITVACEDPYVP 117
 QY 97 VHF 99
 DB 118 VHF 120
 RESULT 14
 RNP_PROGU STANDARD; PRT; 128 AA.
 ID RNP_PROGU
 AC P04059;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 OS Rnase1 OR RNS1.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys.
 CC NCBI_TaxId=101633;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=83000399; PubMed=7115727;
 RA Beutema J.J., Knol G., Martena B.;
 RT "The primary structures of pancreatic ribonucleases from African
 RT porcupine and castor, two hysticomorph rodent species";
 RL Biochim. Biophys. Acta 705:102-110(1982).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00821; NRKS.
 DR HSSP: P00656; ISRN.

Query Match	20.6%;	Score 120;	DB 1;	Length 128;
Best Local Similarity	29.9%;	Pred. No. 4.8e-06;		
Matches 35;	Conservative 18;	Mismatches 36;	Indels 28;	Gaps 7

	RESULT	15
	ANGI_MOUSE	
ID	ANGI_MOUSE	
AC	P21570;	STANDARD; PRT; 145 AA.
AC	P15UVY;1683	157

Characterization and sequencing of rabbit, pig and mouse angiotensins: discernment of functionally important residues and regions."?

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0y	10	KHLTNRDND-----CANNISTNLF-;HCKDKNFTYSRPEPAVC-KGIASKN	57
		back, match	
		20.3%; score 119.5; DB 1;	
		Best Local Similarity	length 145;
		30.8%; Pred. 6.2e-06;	
		Matches	
	33;	Conservative	12; Mismatches 45; Indels 17; Gaps 5;

Search completed: June 25, 2003, 14:50:05
Job time : 6.45349 secs